

Figure 1

09759990 06665460

100E80" 05665460

Stability Study of SAHH

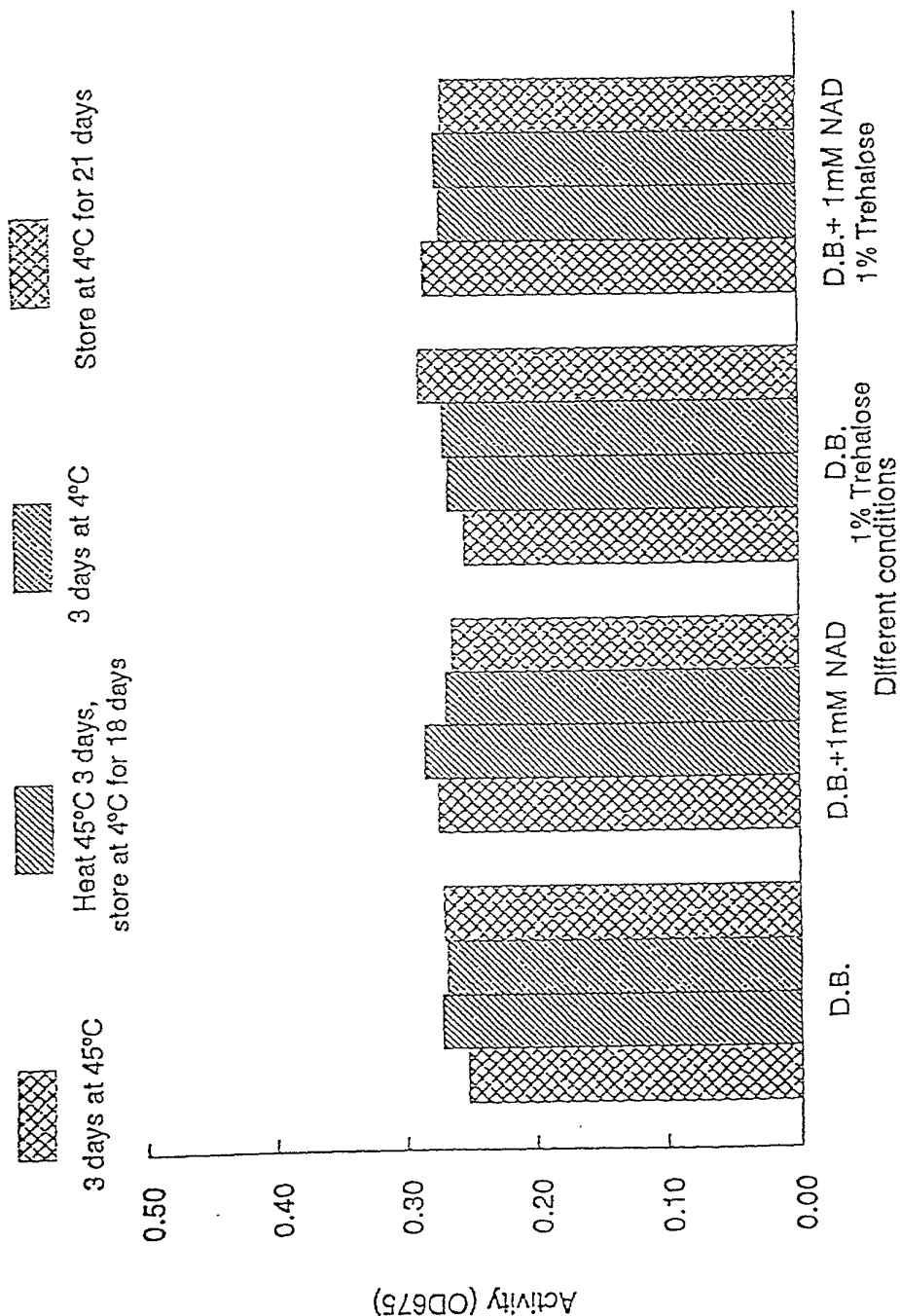


Figure 2

Screening of SAHH

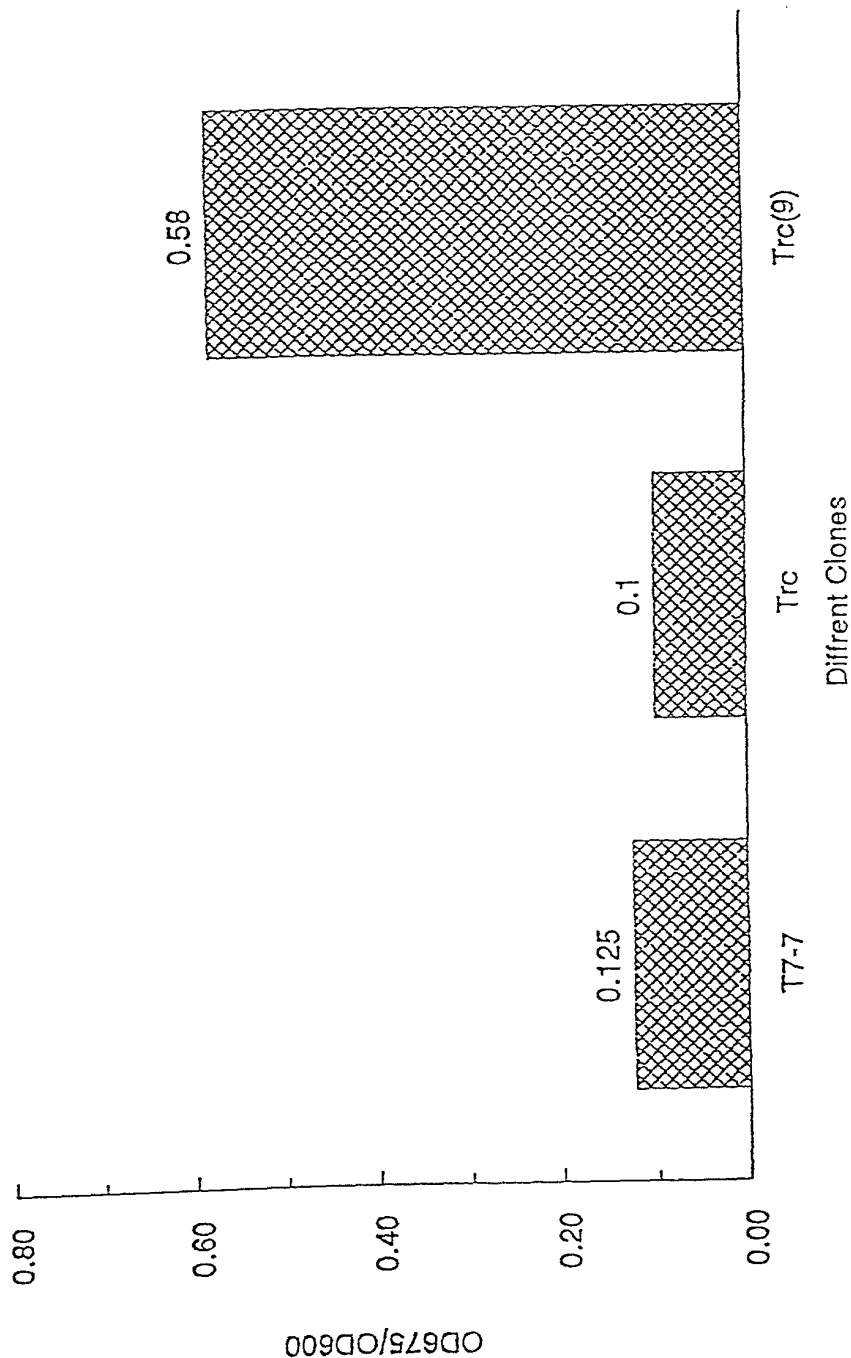


Figure 3

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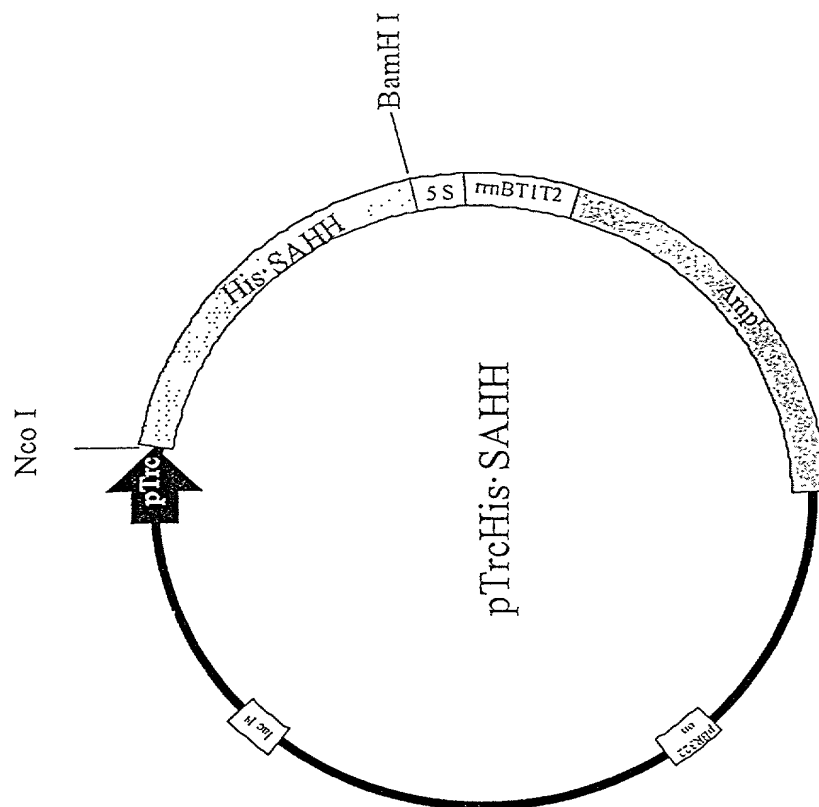


Figure 4

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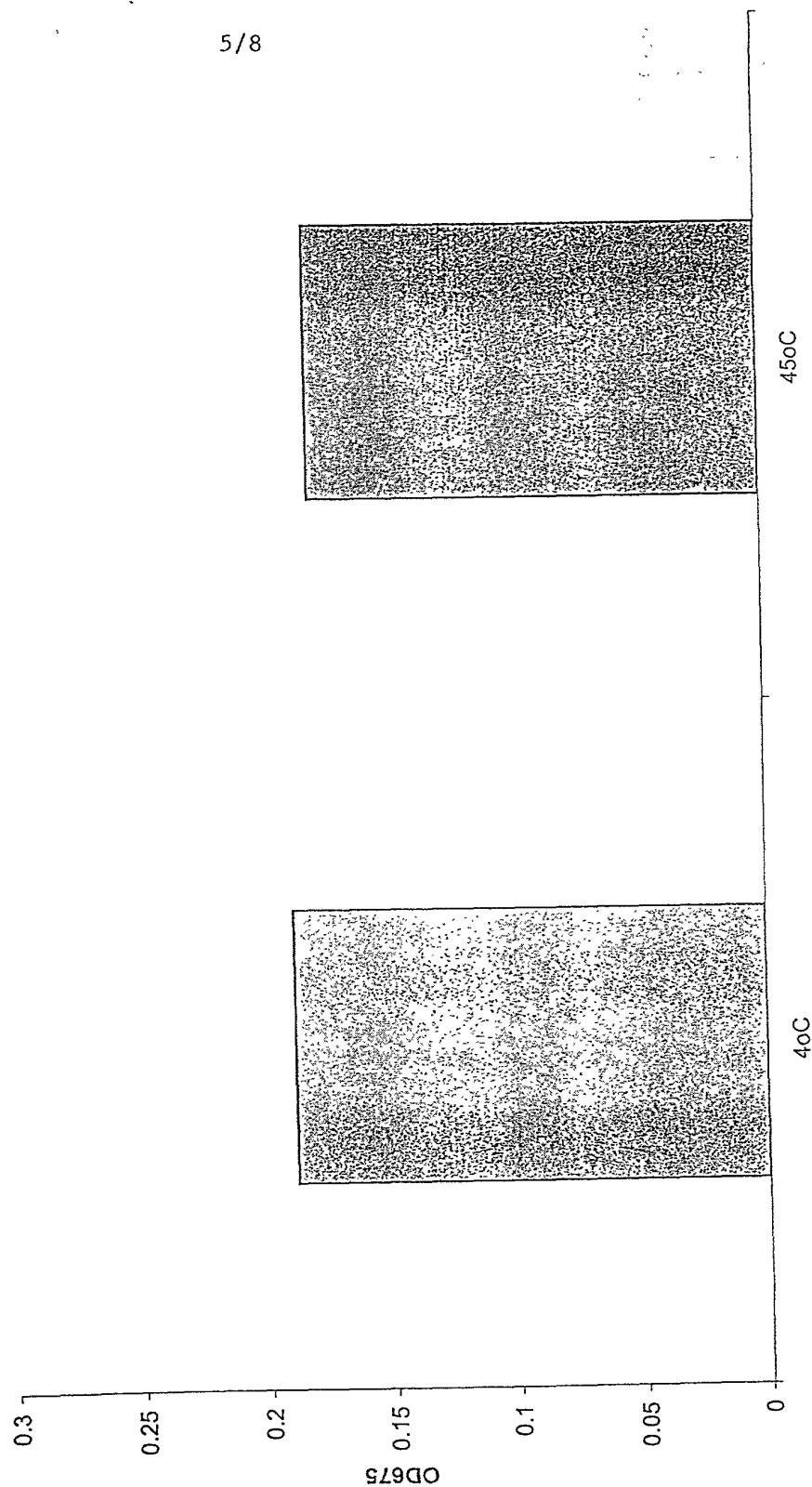


Figure 5

T00E80" 06665.650

Stability of SAHH.His

99.2% identity in 1461 residues overlap; Score: 1437.0; Gap frequency: 0.0%

SAHH-wild	291	ATGGCTTGCAAATCACCTGCTGGTGCTCCATTCGAGTACAGAATTGCCGACATCAACCTC
A/C,	71	ATGGCTTGCAAATCACCTACTGGTGCTCCATTCGAGTACAGAATTGCCGACATCAACCTC

SAHH-wild	351	CATGTTCTCGGCCGTAAGGAACCTTACCCTTGCTGAGAAGGAAATGCCAGGTCTTATGGTT
A/C,	131	CATGTTCTCGGCCGTAAGGAACCTTACCCTTGCTGAGAAGGAAATGCCAGGTCTTATGGTT

SAHH-wild	411	CTTCGTGAGCGTTATTCCGCTTCTAAGCCATTGAAGGGTGTCAGAATCTCTGGTTCCCTC
A/C,	191	CTTCGTGAGCGTTATTCCGCTTCTAAGCCATTGAAGGGTGTCAGAATCTCTGGTTCCCTC

SAHH-wild	471	CACATGACAGTCCAGACAGCGTCTTATTGAGACACTCACAGCTCTTGGTGCTGATGTC
A/C,	251	CACATGACAGTCCAGACAGCGTCTTATTGAGACACTCACAGCTCTTGGTGCTGATGTC

SAHH-wild	531	AGATGGGCTTCCTGCAACATCTTCTCTACACAAGATACAGCCGCTGCTGCTATCGTTGTC
A/C,	311	AGATGGGCTTCCTGCAACATCTTCTCTACACAAGATACAGCCGCTGCTGCTATCGTTGTC

SAHH-wild	591	GGCCCAACAGGCACACCAGAGAAGCCAGCCGGTATCCCAGTCTTCGCCTGGAAGGGCGAA
A/C,	371	GGCCCAACAGGCACACCAGAGAAGCCAGCCGGTATCCCAGTCTTCGCCTGGAAGGGCGAA

SAHH-wild	651	ACACTCCCAGAATACTGGGAGAACACATACCGCGCTCTCACATGGCCAGATGGTCAAGGC
A/C,	431	ACACTCCCAGAATACTGGGAGAACACATACCGCGCTCTCACATGGCCAGATGGTCAAGGC

SAHH-wild	711	CCACAGCAGGTTGTGCGATGATGGTGGTGATGCTACACTCCTCATCTCCAAGGGCTTCGAA
A/C,	491	CCACAGCAGGTTGTGCGATGATGGTGGTGATGCTACACTCCTCATCTCCAAGGGCTTCGAA

SAHH-wild	771	TTCGAAACAGCCGGTGCTGTCCAGAGCCAACAGAAGCTGACAACCTCGAATACCGCTGC
A/C,	551	TTCGAAACAGCCGGTGCTGTCCAGAGCCAACAGAAGCTGACAACCTCGAATACCGCTGC

SAHH-wild	831	GTTCTTGCTACACTCAAGCAGGTCTTCAACCAAGACAAGAACCCTGGCACACAGTTGCT
A/C,	611	GTTCTTGCTACACTCAAGCAGGTCTTCAACCAAGACAAGAACCCTGGCACACAGTTGCT

SAHH-wild	891	GCCGGCATGAACGGTGTTTTCCGAAGAGACAACAACAGGTGTCCACCGCTCTACCAGCTC
A/C,	671	GCCGGCATGAACGGTGTTTTCCGAAGAGACAACAACAGGTGTCCACCGCTCTACCAGCTC

SAHH-wild	951	GAGAAGGAGGGCAAACCTCTTCCAGCCATCAACGTCAACGACGCTGTTACAAAGTCC
A/C,	731	GAGAAGGAGGGCAAACCTCTTCCAGCCATCAACGTCAACGACGCTGTTACAAAGTCC

SAHH-wild	1011	AAGTTCGATAACATCTACGGCTGTCGCCACTCCCTTATCGATGGTATCAACCGTGCTTCC
A/C,	791	AAGTTCGATAACATCTACGGCTGTCGCCACTCCCTTATCGATGGTATCAACCGTGCTTCC

SAHH-wild	1071	GATGTCATGATCGGCGGCAAGACAGCTCTCGTCATGGGTTACGGCGATGTCGGGAAGGGC
A/C,	851	GATGTCATGATCGGCGGCAAGACAGCTCTCGTCATGGGTTACGGCGATGTCGGGAAGGGC

SAHH-wild	1131	TGCGCTCAATCCCTCCGTGGCCAAGGCGCTCGCGTTATCATCACAGAAGTCGACCCATC
A/C,	911	TGCGCTCAATCCCTCCGTGGCCAAGGCGCTCGCGTTATCATCACAGAAGTCGACCCATC

Figure 6a

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SAHH-wild 1191 TCGCTCTCCAGGCTGTCATGGAAGGCTACCAGGTCCGCCGCATCGAGGAAGTCGTCAAG
A/C, 971 TCGCTCTCCAGGCTGCCATGGAAGGCTACCAGGTCCGCCGCATCGAGGAAGTCGTCAAG

SAHH-wild 1251 GATGTCGATATCTTCGTTACATGCACAGGAACTGCGATATCATCTCTGTTGACATGATG
A/C, 1031 GATGTCGATATCTTCGTTACATGCACAGGAACTGCGATATCATCTCTGTTGACATGATG

SAHH-wild 1311 GCCCAGATGAAGGATAAGGCTATTGTGCGTAACATCGGCCACTTCGATAACGAAATTGAT
A/C, 1091 GCCCAGATGAAGGATAAGGCTATTGTGCGTAACATCGGCCACTTCGATAACGAAATTGAT

SAHH-wild 1371 ACAGATGGCCTCATGAAATACCCAGGCATCAAGCACATCCCAATCAAGCCAGAATACGAC
A/C, 1151 ACAGATGGCCTCATGAAATACCCAGGCATCAAGCACATCCCAATCAAGCCAGAATACGAC

SAHH-wildt 1431 ATGTGGGAATTCCCAGATGGCCACGCTATCCTCCTTCTTGCTGAGGGCCGCCTTCTTAAC
A/C, 1211 ATGTGGGAATTCCCAGATGGCCACGCTATCCTCCTTCTTGCTGAGGGCCGCCTTCTTAAC

SAHH-wild 1491 CTTGGTTGCGCTACAGGTCACCCATCTTTCGTTATGTCAATGTCATTACAAACCAGACA
A/C, 1271 CTTGGCTGCGCTACAGGTCACCCATCTTTCGTTATGTCAATGTCATTACAAACCAGACA

SAHH-wild 1551 CTCGCTCAGCTCGACCTCTACGAAAAGAGAGGAAATCTCGAGATGAAGGTTTACACACTT
A/C, 1331 CTCGCTCAGCTCGACCTCTACGAAAAGAGAGGAAATCTCGAGAAGAAGGTTTACACACTT

SAHH-wild 1611 CCGAAGCATCTCGATGAAGAAGTCGTTGCGCTCCACCTCGGATCTCTCGATGTCCACCTT
A/C, 1391 CCGAAGCATCTCGATGAAGAAGTCGTTGCGCTCCACCTCGGATCTCTCGATGTCCACCTT

SAHH-wild 1671 ACAAAGCTTACACAGAAGCAGGCTGACTACATCAACGTTCCAGTTGAGGGTCTTTACAAG
A/C, 1451 ACAAAGCTTACACAGAAGCAGGCTGACTACATCAACGTTCCAGTTGAGGGTCTTTACAAG

SAHH-wild 1731 TCTGATGCTTACCGTTATTAA
A/C, 1511 TCTGATGCTTACCGTTATTAA

65.9% identity in 44 residues overlap; Score: 14.0; Gap frequency: 0.0%

SAHH-wild 782 CGGTGCTGTCCCAGAGCCAACAGAAGCTGACAACCTCGAATACC
A/C, 682 CGGTGTTTCCGAAGAGACAACAACAGGTGTCCACCGCCTCTACC

80.0% identity in 20 residues overlap; Score: 12.0; Gap frequency: 0.0%

SAHH-wild 1053 GGTATCAACCGTGCTTCCGA
A/C, 674 GGCATGAACGGTGTTTCCGA
** ** **

Figure 6b

87.5% identity in 16 residues overlap; Score: 12.0; Gap frequency: 0.0%

SAHH-wild 564 GATACAGCCGCTGCTG
 A/C, 554 GAAACAGCCGGTGCTG
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64.3% identity in 42 residues overlap; Score: 12.0; Gap frequency: 0.0%

SAHH-wild 1224 GTCCGCCGCATCGAGGAAGTCGTCAAGGATGTCGATATCTTC
 A/C, 710 GTCCACCGCCTCTACCAGCTCGAGAAGGAGGGCAAACCTCTC
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87.5% identity in 16 residues overlap; Score: 12.0; Gap frequency: 0.0%

SAHH-wild 774 GAAACAGCCGGTGCTG
 A/C, 344 GATACAGCCGCTGCTG
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Figure 6c

0975990-08300